

10

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ggg Gly 45	tac Tyr	tac Tyr	caa Gln	aat Asn	tac Tyr	caa Gln 50	ggg Gly	tat Tyr	tct Ser	ggg Gly 55	tac Tyr	caa Gln	caa Gln	ggg Gly	ggc Gly	915
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aac Asn	aat Asn 110	ttg Leu	caa Gln	gga Gly	tat Tyr	caa Gln	gct Ala 115	ggg Gly	ttc Phe	caa Gln	cca Pro	cag Gln 120	tct Ser	caa Gln	ggg Gly	1107
atg Met 125	tct Ser	ttg Leu	aac Asn	gac Asp	ttt Phe	caa Gln 130	aag Lys	caa Gln	caa Gln	aag Lys 135	cag Gln	gcc Ala	gct Ala	ccc Pro	aaa Lys	1155
cca Pro 140	aag Lys	aag Lys	act Thr	ttg Leu	aag Lys 145	ctt Leu	gtc Val	tcc Ser	agt Ser	tcc Ser 150	ggg Gly	atc Ile	aag Lys	ttg Leu	gcc Ala 155	1203
aat Asn	gct Ala	acc Thr	aag Lys 160	aag Lys	gtt Val	ggc Gly	aca Thr	aaa Lys	cct Pro 165	gcc Ala	gaa Glu	tct Ser	gat Asp 170	aag Lys	aaa Lys	1251
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acc Thr	gtt Val	aac Asn	tgg Trp 415	tct Ser	aag Lys	gaa Glu	cgt Arg	tac Tyr 420	gac Asp	caa Gln	tgt Cys	gtg Val	agt Ser 425	aat Asn	gtc Val	2019
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aaa Lys	att Ile	gaa Glu 510	tcc Ser	ggt Gly	cat His	atc Ile	aaa Lys 515	aag Lys	ggt Gly	caa Gln	tcc Ser	acc Thr 520	cta Leu	ctg Leu	atg Met	2307

cct Pro	aac Asn	aaa Lys	acc Thr	gct Ala	gtg Val	gaa Glu	att Ile	caa Gln	aat Asn	att Ile	tac Tyr	aac Asn	gaa Glu	act Thr	gaa Glu	2355	
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620						625			630							635	
gct Ala	aag Lys	aag Lys	ggg Gly	atg Met	aag Lys	gtc Val	atc Ile	gct Ala	gtt Val	tta Leu	gaa Glu	act Thr	gaa Glu	gct Ala	cca Pro	2691	
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gcc Ala	gag Glu	taa	atttcttgca	aacataagta	aatgcaaaca	caataatacc										2836	
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gatcataaag ctttttcttc tatattaanaa aacaagggttt aataaagctg ttatatatat 2896																	
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Gln	Ala	Tyr	Asn	Ala	Gln	Ala	Gln	Pro	Ala	Gly	Gly	Tyr	Tyr	Gln	Asn	
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Tyr	Gln	Gly	Tyr	Ser	Gly	Tyr	Gln	Gln	Gly	Gly	Tyr	Gln	Gln	Tyr	Asn	
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Val	Gly	Thr	Lys	Pro	Ala	Glu	Ser	Asp	Lys	Lys	Glu	Glu	Glu	Lys	Ser	
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Ala	Glu	Thr	Lys	Glu	Pro	Thr	Lys	Glu	Pro	Thr	Lys	Val	Glu	Glu	Pro	
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Val	Lys	Lys	Glu	Glu	Lys	Pro	Val	Gln	Thr	Glu	Glu	Lys	Thr	Glu	Glu	
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Glu	Gln	Glu	Glu	Glu	Val	Asp	Asp	Glu	Val	Val	Asn	Asp	Met	Phe	Gly	
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Gly	Lys	Asp	His	Val	Ser	Leu	Ile	Phe	Met	Gly	His	Val	Asp	Ala	Gly	
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Lys	Arg	Thr	Ile	Glu	Lys	Tyr	Glu	Arg	Glu	Ala	Lys	Asp	Ala	Gly	Arg	
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Gln 305	Gly	Trp	Tyr	Leu	Ser 310	Trp	Val	Met	Asp	Thr 315	Asn	Lys	Glu	Glu	Arg 320
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Gln 385	Thr	Arg	Glu	His	Ala 390	Leu	Leu	Ala	Lys	Thr 395	Gln	Gly	Val	Asn	Lys 400
Met	Val	Val	Val	Val 405	Asn	Lys	Met	Asp	Asp 410	Pro	Thr	Val	Asn	Trp 415	Ser
Lys	Glu	Arg	Tyr 420	Asp	Gln	Cys	Val	Ser 425	Asn	Val	Ser	Asn	Phe 430	Leu	Arg
Ala	Ile	Gly 435	Tyr	Asn	Ile	Lys	Thr 440	Asp	Val	Val	Phe	Met 445	Pro	Val	Ser
Gly	Tyr 450	Ser	Gly	Ala	Asn	Leu 455	Lys	Asp	His	Val	Asp 460	Pro	Lys	Glu	Cys
Pro 465	Trp	Tyr	Thr	Gly	Pro 470	Thr	Leu	Leu	Glu	Tyr 475	Leu	Asp	Thr	Met	Asn 480
His	Val	Asp	Arg	His 485	Ile	Asn	Ala	Pro	Phe 490	Met	Leu	Pro	Ile	Ala 495	Ala
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His	Ile	Lys 515	Lys	Gly	Gln	Ser	Thr 520	Leu	Leu	Met	Pro	Asn 525	Lys	Thr	Ala
Val 530	Glu	Ile	Gln	Asn	Ile	Tyr 535	Asn	Glu	Thr	Glu	Asn 540	Glu	Val	Asp	Met
Ala 545	Met	Cys	Gly	Glu	Gln 550	Val	Lys	Leu	Arg	Ile 555	Lys	Gly	Val	Glu	Glu 560
Glu	Asp	Ile	Ser	Pro 565	Gly	Phe	Val	Leu	Thr 570	Ser	Pro	Lys	Asn	Pro 575	Ile
Lys	Ser	Val	Thr 580	Lys	Phe	Val	Ala	Gln 585	Ile	Ala	Ile	Val	Glu 590	Leu	Lys
Ser	Ile	Ile 595	Ala	Ala	Gly	Phe	Ser 600	Cys	Val	Met	His	Val 605	His	Thr	Ala
Ile	Glu 610	Glu	Val	His	Ile	Val 615	Lys	Leu	Leu	His	Lys 620	Leu	Glu	Lys	Gly
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a	atg	atg	aat	aac	aac	ggc	aac	caa	gtg	t	cg	aat	ctc	tcc	aat	gcg	ctc	229
Met	Met	Asn	Asn	Asn	Gly	Asn	Gln	Val	Ser	Asn	Leu	Ser	Asn	Ala	Leu			
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Asn	Asn	Ser	Ser	Ser	Asn	Asn	Asn	Asn	Val	Gln	Asn	Asn	Asn	Asn	Ser	Gly		
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cgc	aat	ggt	agc	caa	aat	aat	gat	aac	gag	aat	aat	atc	aag	aat	acc		421	
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Val	Glu	Tyr	Ser	Arg	Ile	Thr	Lys	Phe	Phe	Gln	Glu	Gln	Pro	Leu	Glu			
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Pro	Met	Ile	Gly	Gln	Ala	Leu	His	Phe	Arg	Tyr	Phe	His	Ser	Gln	Lys		
	225				230					235					240		
ata	gca	agt	gct	gta	gaa	aga	tat	acg	gat	gag	gtt	aga	aga	gtt	tac	949	
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Met	Ser	Gln	Ser	Arg	Phe	Phe	Asp	Tyr	Pro	Val	Trp	Leu	Val	Gly	Asp		
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Asp	Arg	Ile	Gly	Ile	Asn	Ile	Lys	Ile	Glu	Phe	Pro	Glu	Val	Tyr	Lys		
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Trp	Thr	Lys	His	Met	Met	Arg	Arg	Pro	Ala	Val	Ile	Lys	Ala	Leu	Arg		
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Gly	Glu																
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<223> Description of Artificial Sequence: FLAG peptide

<400> 6
Asp Tyr Lys Asp Glu Asp Asp Lys
 1             5

<210> 7
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Strep epitope

<400> 7
Ala Trp Arg His Pro Gln Phe Gly Gly
 1             5

<210> 8
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Hemagglutinin
      epitope

<400> 8
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ile Glu Gly Arg
 1             5             10

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<400> 12
atgtctaaag gtgaagaatt attcactggt gttgtcccaa ttttggttga attagatggt 60
gatgttaatg gtcacaaatt ttctgtctcc ggtgaagggtg aaggatgatgc tacttacggt 120
aaattgacct taaaatttat ttgtactact ggtaaattgc cagttccatg gccaacctta 180
gtcactactt tcggttatgg tgttcaatgt tttgctagat acccagatca tatgaaacaa 240
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<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence
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<400> 13  
tacccatagc acgtcccaga ctacgct 27

<220>  
<223> Description of Artificial Sequence: yeast  
Sup35Rdelta2-5 encoding sequence

<400> 14																
atg	tcg	gat	tca	aac	caa	ggc	aac	aat	cag	caa	aac	tac	cag	caa	tac	48
Met	Ser	Asp	Ser	Asn	Gln	Gly	Asn	Asn	Gln	Gln	Asn	Tyr	Gln	Gln	Tyr	
1				5					10					15		
agc	cag	aac	ggg	aac	caa	caa	caa	ggg	aac	aac	aga	tac	caa	ggg	tat	96
Ser	Gln	Asn	Gly	Asn	Gln	Gln	Gln	Gly	Asn	Asn	Arg	Tyr	Gln	Gly	Tyr	
			20					25					30			
caa	gct	tac	aat	gct	caa	gcc	caa	cct	gca	ggg	ggg	tac	tac	caa	aat	144
Gln	Ala	Tyr	Asn	Ala	Gln	Ala	Gln	Pro	Ala	Gly	Gly	Tyr	Tyr	Gln	Asn	
		35					40					45				

aac ttc aac tac aat aac aat ttg caa gga tat caa gct ggt ttc caa 240  
Asn Phe Asn Tyr Asn Asn Asn Leu Gln Gly Tyr Gln Ala Gly Phe Gln  
65 70 75 80

Gln Ala Ala Pro Lys Pro Lys Lys Thr Leu Lys Leu Val Ser Ser Ser  
100 105 110

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<210> 16
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: yeast
        Sup35R2E2 encoding sequence

<220>
<221> CDS
<222> (1)..(813)

<400> 16
atg tcg gat tca aac caa ggc aac aat cag caa aac tac cag caa tac      48
Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr
   1                    5              10              15

agc cag aac ggt aac caa caa caa ggt aac aac aga tac caa ggt tat      96
Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr
                   20              25              30

caa gct tac aat gct caa gcc caa cct gca ggt ggg tac tac caa aat      144
Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn
   35              40              45

tac caa ggt tat tct ggg tac caa caa ggt ggc tat caa cag tac aat      192
Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn
   50              55              60

ccc caa ggt ggc tat caa cag tac aat ccc caa ggt ggc tat caa cag      240
Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln
   65              70              75              80

tac aat ccc gac gcc ggt tac cag caa cag tat aat cct caa gga ggc      288
Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly
                   85              90              95

tat caa cag tac aat cct caa ggc ggt tat cag cag caa ttc aat cca      336
Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln Gln Phe Asn Pro
   100              105              110

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caa ggt ggc cgt gga aat tac aaa aac ttc aac tac aat aac aat ttg	384
Gln Gly Gly Arg Gly Asn Tyr Lys Asn Phe Asn Tyr Asn Asn Asn Leu	
115 120 125	
caa gga tat caa gct ggt ttc caa cca cag tct caa ggt atg tct ttg	432
Gln Gly Tyr Gln Ala Gly Phe Gln Pro Gln Ser Gln Gly Met Ser Leu	
130 135 140	
aac gac ttt caa aag caa caa aag cag gcc gct ccc aaa cca aag aag	480
Asn Asp Phe Gln Lys Gln Gln Lys Gln Ala Ala Pro Lys Pro Lys Lys	
145 150 155 160	
act ttg aag ctt gtc tcc agt tcc ggt atc aag ttg gcc aat gct acc	528
Thr Leu Lys Leu Val Ser Ser Gly Ile Lys Leu Ala Asn Ala Thr	
165 170 175	
aag aag gtt ggc aca aaa cct gcc gaa tct gat aag aaa gag gaa gag	576
Lys Lys Val Gly Thr Lys Pro Ala Glu Ser Asp Lys Lys Glu Glu Glu	
180 185 190	
aag tct gct gaa acc aaa gaa cca act aaa gag cca aca aag gtc gaa	624
Lys Ser Ala Glu Thr Lys Glu Pro Thr Lys Glu Pro Thr Lys Val Glu	
195 200 205	
gaa cca gtt aaa aag gag gag aaa cca gtc cag act gaa gaa aag acg	672
Glu Pro Val Lys Lys Glu Glu Lys Pro Val Gln Thr Glu Glu Lys Thr	
210 215 220	
gag gaa aaa tcg gaa ctt cca aag gta gaa gac ctt aaa atc tct gaa	720
Glu Glu Lys Ser Glu Leu Pro Lys Val Glu Asp Leu Lys Ile Ser Glu	
225 230 235 240	
tca aca cat aat acc aac aat gcc aat gtt acc agt gct gat gcc ttg	768
Ser Thr His Asn Thr Asn Asn Ala Asn Val Thr Ser Ala Asp Ala Leu	
245 250 255	
atc aag gaa cag gaa gaa gaa gtg gat gac gaa gtt gtt aac gat	813
Ile Lys Glu Gln Glu Glu Glu Val Asp Asp Glu Val Val Asn Asp	
260 265 270	

<210> 17

<211> 271

<212> PRT

<213> Artificial Sequence

<400> 17

Met Ser Asp Ser Asn Gln Gly Asn Asn Gln Gln Asn Tyr Gln Gln Tyr

1

5

10

15

Ser Gln Asn Gly Asn Gln Gln Gln Gly Asn Asn Arg Tyr Gln Gly Tyr

20

25

30

Gln Ala Tyr Asn Ala Gln Ala Gln Pro Ala Gly Gly Tyr Tyr Gln Asn

35

40

45

Tyr Gln Gly Tyr Ser Gly Tyr Gln Gln Gly Gly Tyr Gln Gln Tyr Asn

50

55

60

Pro Gln Gly Gly Tyr Gln Gln Tyr Asn Pro Gln Gly Gly Tyr Gln Gln

65

70

75

80

Tyr Asn Pro Asp Ala Gly Tyr Gln Gln Gln Tyr Asn Pro Gln Gly Gly

<210>	18
<211>	641
<212>	DNA
<213>	MOUSE

<400> 18																
atg	tct	aaa	aag	cgg	cca	aag	cct	gga	ggg	tgg	aac	acc	ggt	gga	agc	48
Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser	
1				5			10					15				
cgg	tat	ccc	ggg	cag	gga	agc	cct	gga	ggc	aac	cgt	tac	cca	cct	cag	96
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln	
20				25					30							
ggt	ggc	acc	tgg	ggg	cag	ccc	cac	ggt	ggt	ggc	tgg	gga	caa	ccc	cat	144
Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	
35				40					45					-----		
ggg	ggc	agc	tgg	gga	caa	cct	cat	ggt	ggt	agt	tgg	ggt	cag	ccc	cat	192
Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	
50				55					60							
ggc	ggt	gga	tgg	ggc	caa	gga	ggg	ggt	acc	cat	aat	cag	tgg	aac	aag	240



Gly	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His	Asn	Gln	Trp	Asn	Lys	
65					70					75					80	
ccc	agc	aaa	cca	aaa	acc	aac	ctc	aag	cat	gtg	gca	ggg	gct	gcg	gca	288
Pro	Ser	Lys	Pro	Lys	Thr	Asn	Leu	Lys	His	Val	Ala	Gly	Ala	Ala	Ala	
				85					90					95		
gct	ggg	gca	gta	gtg	ggg	ggc	ctt	ggt	ggc	tac	atg	ctg	ggg	agc	gcc	336
Ala	Gly	Ala	Val	Val	Gly	Gly	Leu	Gly	Gly	Tyr	Met	Leu	Gly	Ser	Ala	
			100					105					110			
gtg	agc	agg	ccc	atg	atc	cat	ttt	ggc	aac	gac	tgg	gag	gac	cgc	tac	384
Val	Ser	Arg	Pro	Met	Ile	His	Phe	Gly	Asn	Asp	Trp	Glu	Asp	Arg	Tyr	
		115					120					125				
tac	cgt	gaa	aac	atg	tac	cgc	tac	cct	aac	caa	gtg	tac	tac	agg	cca	432
Tyr	Arg	Glu	Asn	Met	Tyr	Arg	Tyr	Pro	Asn	Gln	Val	Tyr	Tyr	Arg	Pro	
	130					135					140					
gtg	gat	cag	tac	agc	aac	cag	aac	aac	ttc	gtg	cac	gac	tgc	gtc	aat	480
Val	Asp	Gln	Tyr	Ser	Asn	Gln	Asn	Asn	Phe	Val	His	Asp	Cys	Val	Asn	
145					150					155					160	
atc	acc	atc	aag	cag	cac	acg	gtc	acc	acc	acc	acc	aag	ggg	gag	aac	528
Ile	Thr	Ile	Lys	Gln	His	Thr	Val	Thr	Thr	Thr	Thr	Lys	Gly	Glu	Asn	
				165				170						175		
ttc	acc	gag	acc	gat	gtg	aag	atg	atg	gag	cgc	gtg	gtg	gag	cag	atg	576
Phe	Thr	Glu	Thr	Asp	Val	Lys	Met	Met	Glu	Arg	Val	Val	Glu	Gln	Met	
			180				185						190			
tgc	gtc	acc	cag	tac	cag	aag	gag	tcc	cag	gcc	tat	tac	gac	ggg	aga	624
Cys	Val	Thr	Gln	Tyr	Gln	Lys	Glu	Ser	Gln	Ala	Tyr	Tyr	Asp	Gly	Arg	
		195					200					205				
aga	tcc	agc	tgataacc													641
Arg	Ser	Ser														
	210															
<210>	19															
<211>	211															
<212>	PRT															
<213>	MOUSE															
<400>	19															
Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser	
1				5				10					15			
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln	
			20					25					30			
Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	
		35					40					45				
Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	Gly	Gly	Ser	Trp	Gly	Gln	Pro	His	
	50					55					60					
Gly	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His	Asn	Gln	Trp	Asn	Lys	
65					70					75					80	
Pro	Ser	Lys	Pro	Lys	Thr	Asn	Leu	Lys	His	Val	Ala	Gly	Ala	Ala	Ala	
				85					90					95		

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<210> 20
<211> 644
<212> DNA
<213> Mesocricetus auratus
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<400> 20																
atg	tct	aag	aag	cgg	cca	aag	cct	gga	ggg	tgg	aac	act	ggc	gga	agc	48
Met	Ser	Lys	Lys	Arg	Pro	Lys	Pro	Gly	Gly	Trp	Asn	Thr	Gly	Gly	Ser	
1				5				10						15		
cga	tac	cct	ggg	cag	ggc	agc	cct	gga	ggc	aac	cgt	tac	cca	cct	cag	96
Arg	Tyr	Pro	Gly	Gln	Gly	Ser	Pro	Gly	Gly	Asn	Arg	Tyr	Pro	Pro	Gln	
		20						25						30		
ggt	ggc	ggc	aca	tgg	ggg	caa	ccc	cat	ggt	ggt	ggc	tgg	gga	cag	ccc	144
Gly	Gly	Gly	Thr	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	
		35				40						45				
cat	ggt	ggt	ggc	tgg	gga	cag	ccc	cat	ggt	ggt	ggc	tgg	ggt	cag	ccc	192
His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	His	Gly	Gly	Gly	Trp	Gly	Gln	Pro	
50						55						60				
cat	ggt	ggt	ggc	tgg	ggt	caa	gga	ggt	ggc	acc	cac	aat	cag	tgg	aac	240
His	Gly	Gly	Gly	Trp	Gly	Gln	Gly	Gly	Gly	Thr	His	Asn	Gln	Trp	Asn	
65				70						75				80		
aag	ccc	agt	aag	cca	aaa	acc	aac	atg	aag	cac	atg	gcc	ggc	gct	gct	288
Lys	Pro	Ser	Lys	Pro	Lys	Thr	Asn	Met	Lys	His	Met	Ala	Gly	Ala	Ala	
				85				90						95		
gcg	gca	ggg	gcc	gtg	gtg	ggg	ggc	ctt	ggt	ggc	tac	atg	ctg	ggg	agt	336
Ala	Ala	Gly	Ala	Val	Val	Gly	Gly	Leu	Gly	Gly	Tyr	Met	Leu	Gly	Ser	
		100						105						110		

Pro Val Asp Gln Tyr Asn Asn Gln Asn Asn Phe Val His Asp Cys Val

<210> 22  
<211> 780  
<212> PRT  
<213> *Saccharomyces cerevisiae*

<400> 22  
Met Lys Lys Lys Asp Asn Ser Asp Asp Lys Asp Asn Val Ala Ser Gly  
1 5 10 15  
Gly Tyr Lys Asn Ala Ala Asp Ala Gly Ser Asn Asn Ala Ser Lys Lys  
20 25 30  
Ser Ser Tyr Arg Asn Trp Lys Gly Gly Asn Tyr Gly Gly Tyr Ser Tyr  
35 40 45  
Asn Ser Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr Asn Asn Tyr  
50 55 60  
Asn Asn Tyr Asn Asn Tyr Asn Lys Tyr Asn Gly Gly Tyr Lys Ser Thr  
65 70 75 80  
Tyr Lys Ser Ala Val Thr Asn Ser Gly Thr Thr Ser Ala Ser Thr Thr  
85 90 95  
Ser Thr Ser Asn Lys Ser Asn Thr Ser Ser Lys Cys Ser Thr Asp Cys  
100 105 110  
Lys Asn Lys Gly Lys Gly Asn Ser Thr Gly Lys Trp Lys Val Asp Val  
115 120 125  
Ser Lys Lys Lys Asn Ser Val Arg Ser Ala Met Ser Asn Ala Ser Gly  
130 135 140  
Lys Ala Tyr Asn Val Ala Asp Cys Ser Asp Lys Asn Thr Val Lys Arg  
145 150 155 160  
Ala Ala His Ala Asp Ser Asn Cys Met Ala Thr Cys Val Thr Asp Tyr  
165 170 175  
Ser Ser Gly Ala Lys Trp Ala Lys Met Ala Ala Ser Val Val Asp Arg  
180 185 190  
Arg Asp Ser Ala Asn Asp Thr Lys Asp Ala Val Val Thr Asp Val Ala  
195 200 205  
Thr Asp Lys Ala Lys Gly Tyr Lys Thr Asp Tyr Val Ser Asp Asn Asp  
210 215 220

Ser 225	Arg	Tyr	Lys	Val	Asp 230	Thr	Asp	Ser	Lys	Val 235	Ser	Val	Lys	Ser	Ser 240
Ser	Val	Thr	Val	Ala 245	Val	Thr	Ser	Ser	Val 250	Asn	Arg	Ser	Asn	Ser	Ser 255
Ser	Ser	Arg	Thr 260	Val	Val	Val	Asn	Thr 265	Arg	Val	Asn	Asn	Arg 270	Asn	Ser 275
Gly	Lys	Val 275	Val	Asp	Thr	Ala	Ser 280	Val	Arg	Ala	Lys	Ala 285	Asn	Val	Lys 290
Asp 290	Ala	Asp	Lys	Asn	Lys 295	Ser	Gly	Arg	Thr	Gly 300	Arg	Asp	Asp	His	His 305
Lys 305	Asp	Lys	Ala	Asp	Asp 310	Ser	Cys	Val	Lys	Tyr 315	Met	Asn	Asp	Thr	Val 320
Lys	Tyr	Met	Ser	Lys 325	Thr	Val	Asp	Ser	Asn 330	Val	Asn	Asp	Trp	Lys 335	Arg 340
Asp	Thr	Ala 340	Val	Gly	Gly	Ser	Asp 345	Ser	Arg	Val	Lys	Asp	His 350	Asn	Arg 355
Ala	Tyr	Lys 355	Arg	Ala	Asp	Asp	Gly 360	Val	Asn	Thr	Asp	Ser 365	Ala	Tyr	Gly 370
Ser	Arg 370	Met	Asn	Lys	Thr	Asn 375	Arg	Lys	Gly	His	Arg 380	Tyr	Gly	Cys	Gly 385
Arg 385	Asn	Gly	Ala	Gly	Lys 390	Ser	Thr	Met	Arg	Ala 395	Ala	Asn	Gly	Asp	Gly 400
Asp	Lys	Asp	Thr	Arg 405	Thr	Cys	Val	His	Lys 410	Gly	Gly	Asp	Asp	Val 415	Ser 420
Ala	Asp	Ser	Thr 420	Ser	Arg	Ala	Ala 425	Ala	Ser	Val	Gly	Asp	Arg 430	Arg	Ala 435
Thr	Val	Gly 435	Ser	Ser	Gly	Gly	Trp 440	Lys	Met	Lys	Ala	Arg 445	Ala	Met	Lys 450
Ala 450	Asp	Asp	Thr	Asn	His 455	Asp	Val	Ser	Asn	Val	Lys 460	Trp	Tyr	His	Thr 465
Asp 465	Thr	Ser	Val	Ser	His 470	Asp	Ser	Gly	Asp	Thr 475	Val	Cys	Thr	Asp	His 480
Tyr	Asn	Lys	Lys 485	Ala	Tyr	Tyr	Lys	Gly	Asn 490	Ala	Ala	Val	Lys	Ala 495	Lys 500
Ser	Tyr	Tyr	Thr 500	Thr	Asp	Ser	Asn	Ala 505	Met	Arg	Gly	Thr	Gly 510	Val	Lys 515
Ser	Asn	Thr 515	Arg	Ala	Val	Ala	Lys 520	Met	Thr	Asp	Val	Thr 525	Ser	Tyr	Gly 530
Ala	Lys 530	Ser	Ser	His	Val	Ser 535	Cys	Ser	Ser	Ser	Ser 540	Arg	Val	Ala	Cys 545
Gly 545	Asn	Gly	Ala	Gly	Lys 550	Ser	Thr	Lys	Thr	Gly 555	Val	Asn	Gly	Lys	Val 560

Lys His Asn Arg Gly Tyr Ala His Ala His Val Asn His Lys Lys Thr  
565 570 575

Ala Asn Tyr Trp Arg Tyr Gly Asp Asp Arg Val Lys Ser Arg Lys Ser  
580 585 590

Asp Lys Met Met Thr Lys Asp Asp Asp Gly Arg Gly Lys Arg Ala Ala  
595 600 605

Val Gly Arg Lys Lys Lys Ser Tyr Val Lys Trp Lys Tyr Trp Lys Lys  
610 615 620

Tyr Asn Ser Trp Val Lys Asp Val Val His Gly Lys Val Lys Asp Asp  
625 630 635 640

His Ala Ser Arg Gly Gly Tyr Arg Ser Val Thr Lys His Asp Val Gly  
645 650 655

Asp Ser Ala Asn His Thr Gly Ser Ser Gly Gly Val Lys Val Val Ala  
660 665 670

Gly Ala Met Trp Asn Asn His Val Asp Thr Asn Tyr Asp Arg Asp Ser  
675 680 685

Gly Ala Ala Val Ala Arg Asp Trp Ser Gly Gly Val Val Met Ser His  
690 695 700

Asn Asn Val Gly Ala Cys Trp Val Asn Gly Lys Met Val Lys Gly Ser  
705 710 715 720

Ala Val Asp Ser Lys Asp Gly Gly Asn Ala Asp Ala Val Gly Lys Ala  
725 730 735

Ser Asn Ala Lys Ser Val Asp Asp Asp Asp Ser Ala Asn Lys Val Lys  
740 745 750

Arg Lys Lys Arg Thr Arg Asn Lys Lys Ala Arg Arg Arg Tyr Trp  
755 760 765

Ser Ser Lys Gly Thr Lys Val Asp Thr Asp Asp Asp  
770 775 780

<210> 23

<211> 1075

<212> PRT

<213> Saccharomyces cerevisiae

<400> 23

Met Asp Asn Lys Arg Leu Tyr Asn Gly Asn Leu Ser Asn Ile Pro Glu  
1 5 10 15

Val Ile Asp Pro Gly Ile Thr Ile Pro Ile Tyr Glu Glu Asp Ile Arg  
20 25 30

Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val Ser Asp  
35 40 45

Lys Arg Gly Arg Ser Ser Ser Thr Ser Pro Gln Lys Ile Gly Ser Tyr  
50 55 60

Arg Thr Arg Ala Gly Arg Phe Ser Asp Thr Leu Thr Asn Leu Leu Pro  
65 70 75 80

Ser	Ile	Ser	Ala	Lys 85	Leu	His	His	Ser	Lys 90	Lys	Ser	Thr	Pro	Val 95	Val
Val	Val	Pro	Pro 100	Thr	Ser	Ser	Thr	Pro 105	Asp	Ser	Leu	Asn	Ser 110	Thr	Thr
Tyr	Ala	Pro 115	Arg	Val	Ser	Ser	Asp 120	Ser	Phe	Thr	Val	Ala 125	Thr	Pro	Leu
Ser	Leu 130	Gln	Ser	Thr	Thr	Thr	Arg 135	Thr	Arg	Thr	Arg 140	Asn	Asn	Thr	Val
Ser 145	Ser	Gln	Ile	Thr 150	Ala	Ser	Ser	Ser	Leu 155	Thr	Thr	Asp	Val	Gly	Asn 160
Ala	Thr	Ser	Ala	Asn 165	Ile	Trp	Ser	Ala	Asn 170	Ala	Glu	Ser	Asn	Thr 175	Ser
Ser	Ser	Pro	Leu 180	Phe	Asp	Tyr	Pro	Leu 185	Ala	Thr	Ser	Tyr	Phe 190	Glu	Pro
Leu	Thr	Arg 195	Phe	Lys	Ser	Thr	Asp 200	Asn	Tyr	Thr	Leu	Pro 205	Gln	Thr	Ala
Gln	Leu 210	Asn	Ser	Phe	Leu	Glu 215	Lys	Asn	Gly	Asn	Pro 220	Asn	Ile	Trp	Ser
Ser 225	Ala	Gly	Asn	Ser	Asn 230	Thr	Asp	His	Leu	Asn 235	Thr	Pro	Ile	Val	Asn 240
Arg	Gln	Arg	Ser	Gln 245	Ser	Gln	Ser	Thr	Thr 250	Asn	Arg	Val	Tyr	Thr 255	Asp
Ala	Pro	Tyr	Tyr 260	Gln	Gln	Pro	Ala	Gln 265	Asn	Tyr	Gln	Val	Gln	Val	Pro
Pro	Arg	Val 275	Pro	Lys	Ser	Thr	Ser 280	Ile	Ser	Pro	Val	Ile 285	Leu	Asp	Asp
Val	Asp 290	Pro	Ala	Ser	Ile	Asn 295	Trp	Ile	Thr	Ala	Asn 300	Gln	Lys	Val	Pro
Leu 305	Val	Asn	Gln	Ile	Ser	Ala	Leu	Leu	Pro	Thr 315	Asn	Thr	Ile	Ser	Ile 320
Ser	Asn	Val	Phe	Pro 325	Leu	Gln	Pro	Thr	Gln 330	Gln	His	Gln	Gln	Asn 335	Ala
Val	Asn	Leu	Thr 340	Ser	Thr	Ser	Leu	Ala 345	Thr	Leu	Cys	Ser	Gln 350	Tyr	Gly
Lys	Val	Leu 355	Ser	Ala	Arg	Thr	Leu 360	Arg	Gly	Leu	Asn	Met 365	Ala	Leu	Val
Glu	Phe 370	Ser	Thr	Val	Glu	Ser 375	Ala	Ile	Cys	Ala	Leu 380	Glu	Ala	Leu	Gln
Gly 385	Lys	Glu	Leu	Ser	Lys 390	Val	Gly	Ala	Pro	Ser 395	Thr	Val	Ser	Phe	Ala 400
Arg	Val	Leu	Pro	Met 405	Tyr	Glu	Gln	Pro	Leu 410	Asn	Val	Asn	Gly	Phe 415	Asn

Asn	Thr	Pro	Lys 420	Gln	Pro	Leu	Leu	Gln	Glu	Gln	Leu	Asn	His 430	Gly	Val
Leu	Asn	Tyr 435	Gln	Leu	Gln	Gln	Ser 440	Leu	Gln	Gln	Pro	Glu 445	Leu	Gln	Gln
Gln	Pro	Thr 450	Ser	Phe	Asn	Gln 455	Pro	Asn	Leu	Thr	Tyr 460	Cys	Asn	Pro	Thr
Gln 465	Asn	Leu	Ser	His	Leu 470	Gln	Leu	Ser	Ser	Asn 475	Glu	Asn	Glu	Pro	Tyr 480
Pro	Phe	Pro	Leu	Pro 485	Pro	Pro	Ser	Leu	Ser 490	Asp	Ser	Lys	Lys	Asp 495	Ile
Leu	His	Thr	Ile 500	Ser	Ser	Phe	Lys 505	Leu	Glu	Tyr	Asp	His	Leu 510	Glu	Leu
Asn	His	Leu 515	Leu	Gln	Asn	Ala 520	Leu	Lys	Asn	Lys	Gly 525	Val	Ser	Asp	Thr
Asn	Tyr 530	Phe	Gly	Pro	Leu	Pro 535	Glu	His	Asn	Ser	Lys 540	Val	Pro	Lys	Arg
Lys 545	Asp	Thr	Phe	Asp	Ala 550	Pro	Lys	Leu	Arg	Glu 555	Leu	Arg	Lys	Gln	Phe 560
Asp	Ser	Asn	Ser	Leu 565	Ser	Thr	Ile	Glu	Met 570	Glu	Gln	Leu	Ala	Ile 575	Val
Met	Leu	Asp	Gln 580	Leu	Pro	Glu	Leu	Ser 585	Ser	Asp	Tyr	Leu	Gly 590	Asn	Thr
Val	Ile	Gln 595	Lys	Leu	Phe	Glu	Asn 600	Ser	Ser	Asn	Ile	Ile 605	Arg	Asp	Ile
Met 610	Leu	Arg	Lys	Cys	Asn 615	Lys	Tyr	Leu	Thr	Ser 620	Met	Gly	Val	His	Lys
Asn 625	Gly	Thr	Trp	Val	Cys 630	Gln	Lys	Ile	Ile	Lys 635	Met	Ala	Asn	Thr	Pro 640
Arg	Gln	Ile	Asn 645	Leu	Val	Thr	Ser	Gly	Val 650	Ser	Asp	Tyr	Cys	Thr 655	Pro
Leu	Phe	Asn	Asp 660	Gln	Phe	Gly	Asn 665	Tyr	Val	Ile	Gln	Gly	Ile 670	Leu	Lys
Phe	Gly	Phe 675	Pro	Trp	Asn	Ser	Phe 680	Ile	Phe	Glu	Ser 685	Val	Leu	Ser	His
Phe 690	Trp	Thr	Ile	Val	Gln	Asn 695	Arg	Tyr	Gly	Ser	Arg 700	Ala	Val	Arg	Ala
Cys 705	Leu	Glu	Ala	Asp 710	Ser	Ile	Ile	Thr	Gln 715	Cys	Gln	Leu	Leu	Thr	Ile 720
Thr	Ser	Leu	Ile 725	Ile	Val	Leu	Ser	Pro	Tyr 730	Leu	Ala	Thr	Asp	Thr 735	Asn
Gly	Thr	Leu 740	Leu	Ile	Thr	Trp	Leu 745	Leu	Asp	Thr	Cys	Thr 750	Leu	Pro	Asn



Lys Asn Leu Ile Leu Cys Asp Lys Leu Val Asn Lys Asn Leu Val Lys  
 755 760 765  
 Leu Cys Cys His Lys Leu Gly Ser Leu Thr Val Leu Lys Ile Leu Asn  
 770 775 780  
 Leu Arg Gly Gly Glu Glu Glu Ala Leu Ser Lys Asn Lys Ile Ile His  
 785 790 795 800  
 Ala Ile Phe Asp Gly Pro Ile Ser Ser Asp Ser Ile Leu Phe Gln Ile  
 805 810 815  
 Leu Asp Glu Gly Asn Tyr Gly Pro Thr Phe Ile Tyr Lys Val Leu Thr  
 820 825 830  
 Ser Arg Ile Leu Asp Asn Ser Val Arg Asp Glu Ala Ile Thr Lys Ile  
 835 840 845  
 Arg Gln Leu Ile Leu Asn Ser Asn Ile Asn Leu Gln Ser Arg Gln Leu  
 850 855 860  
 Leu Glu Glu Val Gly Leu Ser Ser Ala Gly Ile Ser Pro Lys Gln Ser  
 865 870 875 880  
 Ser Lys Asn His Arg Lys Gln His Pro Gln Gly Phe His Ser Pro Gly  
 885 890 895  
 Arg Ala Arg Gly Val Ser Val Ser Ser Val Arg Ser Ser Asn Ser Arg  
 900 905 910  
 His Asn Ser Val Ile Gln Met Asn Asn Ala Gly Pro Thr Pro Ala Leu  
 915 920 925  
 Asn Phe Asn Pro Ala Pro Met Ser Glu Ile Asn Ser Tyr Phe Asn Asn  
 930 935 940  
 Gln Gln Val Val Tyr Ser Gly Asn Gln Asn Gln Asn Gln Asn Gly Asn  
 945 950 955 960  
 Ser Asn Gly Leu Asp Glu Leu Asn Ser Gln Phe Asp Ser Phe Arg Ile  
 965 970 975  
 Ala Asn Gly Thr Asn Leu Ser Leu Pro Ile Val Asn Leu Pro Asn Val  
 980 985 990  
 Ser Asn Asn Asn Asn Asn Tyr Asn Asn Ser Gly Tyr Ser Ser Gln Met  
 995 1000 1005  
 Asn Pro Leu Ser Arg Ser Val Ser His Asn Asn Asn Asn Asn Thr Asn  
 1010 1015 1020  
 Asn Tyr Asn Asn Asn Asp Asn Asp Asn Asn Asn Asn Asn Asn Asn  
 1025 1030 1035 1040  
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn  
 1045 1050 1055  
 Ser Asn Asn Asn Asn Asn Asn Asn Asp Thr Ser Leu Tyr Arg Tyr Arg Ser  
 1060 1065 1070  
 Tyr Gly Tyr  
 1075

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<400> 24
Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Lys Ser Tyr Ser
  1                    5                10              15

Arg Ser Asn Ser Ser Ala His Asn Lys Thr Arg Gly Tyr Tyr Tyr His
          20                25              30

Gly Tyr Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn Gly Tyr Asn
      35                40              45

Gly Tyr Asn Gly Tyr Asn Gly His Val Tyr Val Arg Gly Asn Gly Cys
      50                55              60

Ala Ala Cys Ala Ala Cys Cys Thr Met Asp Met
  65                70              75

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<210> 25
<211> 380
<212> PRT
<213> Saccharomyces cerevisiae

<400> 25
Met Ser Ser Asp Asp Asn Asp Tyr Gly Asp Asp Lys Thr Thr Thr Val
  1          5          10          15
Lys Lys Asn Lys Ala Gly Ser Gly Thr Ser Asp Ala Ala Ala Ser Ser
  20          25          30
Ser Asn Lys Asn Asn Asn Ser Asn Asn Ser Ser Ser Asn Asn Ser Asn
  35          40          45
Asp Thr Ser Ser Ser Lys Asp Gly Thr Ala Asn Asp Lys Gly Ser Asn
  50          55          60
Asp Thr Lys Asn Lys Lys Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn
  65          70          75          80
Ala Ser Ser Ala Gly Ser Gly Trp Thr Met Ser Ser Ser Ser Val Thr
  85          90          95
Thr Lys Arg Ser Lys Ala Asp Ser Lys Ser Cys Lys Met Gly Gly Asn
  100          105          110
Trp Asp Thr Thr Asp Asn Arg Tyr Gly Lys Tyr Gly Thr Val Thr Asp
  115          120          125
Lys Met Lys Asp Ala Thr Gly Arg Ser Arg Gly Gly Ser Lys Ser Ser
  130          135          140
Val Asp Val Val Lys Thr His Asp Gly Lys Val Asp Lys Arg Ala Arg
145-----150-----155-----160
Asp Asp Lys Thr Gly Lys Val Gly Gly Gly Asp Val Arg Lys Ser Trp
  165          170          175
Gly Thr Asp Ala Met Asp Lys Asp Thr Gly Ser Arg Gly Gly Val Thr
  180          185          190

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Thr Met Lys Asn Gly Cys Ser Trp Asp Lys Asp Ala Arg Asn Ser Thr  
100 105 110

Thr Ser Ser Val Asn Thr Arg Asp Asp Gly Thr Gly Ala Ser Val Ala  
115 120 125

Arg Asn Asn Arg Gly Ser Val Thr Val Arg Asp Asp Asn Arg Arg Ser  
130 135 140

Asn Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg  
145 150 155 160

Gly Gly Ser Arg Gly Gly Gly Gly Arg Gly Gly Gly Gly Arg Gly Gly  
165 170 175

Tyr Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Tyr Ser Arg Gly Gly  
180 185 190

Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Ser Arg Gly Gly Tyr Asp Ser  
195 200 205

Arg Gly Gly Tyr Ser Arg Gly Gly Tyr Gly Gly Arg Asn Asp Tyr Gly  
210 215 220

Arg Gly Ser Tyr Gly Gly Ser Arg Gly Gly Tyr Asp Gly Arg Gly Asp  
225 230 235 240

Tyr Gly Arg Asp Ala Tyr Arg Thr Arg Asp Ala Arg Arg Ser Thr Arg  
245 250 255

<210> 27  
<211> 286  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 27  
Met Ser Asp Ile Glu Glu Gly Thr Pro Thr Asn Asn Gly Gln Gln Lys  
1 5 10 15

Glu Arg Arg Lys Ile Glu Ile Lys Phe Ile Glu Asn Lys Thr Arg Arg  
20 25 30

His Val Thr Phe Ser Lys Arg Lys His Gly Ile Met Lys Lys Ala Phe  
35 40 45

Glu Leu Ser Val Leu Thr Gly Thr Gln Val Leu Leu Leu Val Val Ser  
50 55 60

Glu Thr Gly Leu Val Tyr Thr Phe Ser Thr Pro Lys Phe Glu Pro Ile  
65 70 75 80

Val Thr Gln Gln Glu Gly Arg Asn Leu Ile Gln Ala Cys Leu Asn Ala  
85 90 95

Pro Asp Asp Glu Glu Glu Asp Glu Glu Glu Asp Gly Asp Asp Asp Asp  
100 105 110

Asp Asp Asp Asp Asp Gly Asn Asp Met Gln Arg Gln Gln Pro Gln Gln  
115 120 125

Gln Gln Pro Gln Gln Gln Gln Gln Val Leu Asn Ala His Ala Asn Ser  
130 135 140

Asp Ala Glu Glu Glu Glu Asp Glu Glu Ser Ser Asn Lys Lys Gln Lys  
145 150 155 160

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<210> 29
<211> 405
<212> PRT
<213> Saccharomyces cerevisiae
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Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys  
35 40 45

Ile	Ala	Gly	Tyr	Val	Met	Asp	Asn	Arg	Ser	Gly	Gly	Ser	Asp	Ala	Ser
50						55					60				
Gln	Asp	Arg	Ala	Ala	Gly	Gly	Gly	Ser	Ser	Phe	Met	Asn	Thr	Leu	Met
65					70					75					80
Ala	Asp	Ser	Lys	Gly	Ser	Ser	Gln	Thr	Gln	Leu	Gly	Lys	Leu	Ala	Leu
				85					90					95	
Leu	Ala	Thr	Val	Met	Thr	His	Ser	Ser	Asn	Lys	Gly	Ser	Ser	Asn	Arg
			100					105					110		
Gly	Phe	Asp	Val	Gly	Thr	Val	Met	Ser	Met	Leu	Ser	Gly	Ser	Gly	Gly
		115					120					125			
Gly	Ser	Gln	Ser	Met	Gly	Ala	Ser	Gly	Leu	Ala	Ala	Leu	Ala	Ser	Gln
						135					140				
Phe	Phe	Lys	Ser	Gly	Asn	Asn	Ser	Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly
145					150					155					160
Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly	Gln	Gly	Ser	Phe	Thr	Ala
				165					170					175	
Leu	Ala	Ser	Leu	Ala	Ser	Ser	Phe	Met	Asn	Ser	Asn	Asn	Asn	Asn	Gln
			180					185					190		
Gln	Gly	Gln	Asn	Gln	Ser	Ser	Gly	Gly	Ser	Ser	Phe	Gly	Ala	Leu	Ala
			195				200					205			
Ser	Met	Ala	Ser	Ser	Phe	Met	His	Ser	Asn	Asn	Asn	Gln	Asn	Ser	Asn
						215					220				
Asn	Ser	Gln	Gln	Gly	Tyr	Asn	Gln	Ser	Tyr	Gln	Asn	Gly	Asn	Gln	Asn
225					230					235					240
Ser	Gln	Gly	Tyr	Asn	Asn	Gln	Gln	Tyr	Gln	Gly	Gly	Asn	Gly	Gly	Tyr
				245					250					255	
Gln	Gln	Gln	Gln	Gly	Gln	Ser	Gly	Gly	Ala	Phe	Ser	Ser	Leu	Ala	Ser
				260				265					270		
Met	Ala	Gln	Ser	Tyr	Leu	Gly	Gly	Gly	Gln	Thr	Gln	Ser	Asn	Gln	Gln
				275			280					285			
Gln	Tyr	Asn	Gln	Gln	Gly	Gln	Asn	Asn	Gln	Gln	Gln	Tyr	Gln	Gln	Gln
						295					300				
Gly	Gln	Asn	Tyr	Gln	His	Gln	Gln	Gln	Gly	Gln	Gln	Gln	Gln	Gln	Gly
305					310					315					320
His	Ser	Ser	Ser	Phe	Ser	Ala	Leu	Ala	Ser	Met	Ala	Ser	Ser	Tyr	Leu
				325					330					335	
Gly	Asn	Asn	Ser	Asn	Ser	Asn	Ser	Ser	Tyr	Gly	Gly	Gln	Gln	Gln	Ala
				340				345					350		
Asn	Glu	Tyr	Gly	Arg	Pro	Gln	His	Asn	Gly	Gln	Gln	Gln	Ser	Asn	Glu
							360					365			
Tyr	Gly	Arg	Pro	Gln	Tyr	Gly	Gly	Asn	Gln	Asn	Ser	Asn	Gly	Gln	His
						375					380				

Asn Gln Asn Arg Tyr  
405

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<210> 30
<211> 964
<212> PRT
<213> Saccharomyces cerevisiae
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Val Thr Arg Ala Cys Asp Glu Cys Arg Lys Lys Lys Val Lys Cys Asp  
20 25 30

Gly Gln Gln Pro Cys Ile His Cys Thr Val Tyr Ser Tyr Glu Cys Thr  
35 40 45

Tyr Lys Lys Pro Thr Lys Arg Thr Gln Asn Ser Gly Asn Ser Gly Val  
50 55 60

Leu Thr Leu Gly Asn Val Thr Thr Gly Pro Ser Ser Ser Thr Val Val  
65 70 75 80

Ala Ala Ala Ala Ser Asn Pro Asn Lys Leu Leu Ser Asn Ile Lys Thr  
85 90 95

Glu Arg Ala Ile Leu Pro Gly Ala Ser Thr Ile Pro Ala Ser Asn Asn  
100 105 110

Pro Ser Lys Pro Arg Lys Tyr Lys Thr Lys Ser Thr Arg Leu Gln Ser  
115 120 125

Lys Ile Asp Arg Tyr Lys Gln Ile Phe Asp Glu Val Phe Pro Gln Leu  
130 135 140

Pro Asp Ile Asp Asn Leu Asp Ile Pro Val Phe Leu Gln Ile Phe His  
145 150 155 160

Asn Phe Lys Arg Asp Ser Gln Ser Phe Leu Asp Asp Thr Val Lys Glu  
165 170 175

Tyr Thr Leu Ile Val Asn Asp Ser Ser Ser Pro Ile Gln Pro Val Leu  
180 185 190

Ser Ser Asn Ser Lys Asn Ser Thr Pro Asp Glu Phe Leu Pro Asn Met  
195 200 205

Lys Ser Asp Ser Asn Ser Ala Ser Ser Asn Arg Glu Gln Asp Ser Val  
210 215 220

Asp Thr Tyr Ser Asn Ile Pro Val Gly Arg Glu Ile Lys Ile Ile Leu  
225-----230-----235-----240

Pro Pro Lys Ala Ile Ala Leu Gln Phe Val Lys Ser Thr Trp Glu His  
245 250 255

Cys Cys Val Leu Leu Arg Phe Tyr His Arg Pro Ser Phe Ile Arg Gln  
260 265 270



Leu Asp Glu Leu Tyr Glu Thr Asp Pro Asn Asn Tyr Thr Ser Lys Gln  
 275 280 285  
 Met Gln Phe Leu Pro Leu Cys Tyr Ala Ala Ile Ala Val Gly Ala Leu  
 290 295 300  
 Phe Ser Lys Ser Ile Val Ser Asn Asp Ser Ser Arg Glu Lys Phe Leu  
 305 310 315 320  
 Gln Asp Glu Gly Tyr Lys Tyr Phe Ile Ala Ala Arg Lys Leu Ile Asp  
 325 330 335  
 Ile Thr Asn Ala Arg Asp Leu Asn Ser Ile Gln Ala Ile Leu Met Leu  
 340 345 350  
 Ile Ile Phe Leu Gln Cys Ser Ala Arg Leu Ser Thr Cys Tyr Thr Tyr  
 355 360 365  
 Ile Gly Val Ala Met Arg Ser Ala Leu Arg Ala Gly Phe His Arg Lys  
 370 375 380  
 Leu Ser Pro Asn Ser Gly Phe Ser Pro Ile Glu Ile Glu Met Arg Lys  
 385 390 395 400  
 Arg Leu Phe Tyr Thr Ile Tyr Lys Leu Asp Val Tyr Ile Asn Ala Met  
 405 410 415  
 Leu Gly Leu Pro Arg Ser Ile Ser Pro Asp Asp Phe Asp Gln Thr Leu  
 420 425 430  
 Pro Leu Asp Leu Ser Asp Glu Asn Ile Thr Glu Val Ala Tyr Leu Pro  
 435 440 445  
 Glu Asn Gln His Ser Val Leu Ser Ser Thr Gly Ile Ser Asn Glu His  
 450 455 460  
 Thr Lys Leu Phe Leu Ile Leu Asn Glu Ile Ile Ser Glu Leu Tyr Pro  
 465 470 475 480  
 Ile Lys Lys Thr Ser Asn Ile Ile Ser His Glu Thr Val Thr Ser Leu  
 485 490 495  
 Glu Leu Lys Leu Arg Asn Trp Leu Asp Ser Leu Pro Lys Glu Leu Ile  
 500 505 510  
 Pro Asn Ala Glu Asn Ile Asp Pro Glu Tyr Glu Arg Ala Asn Arg Leu  
 515 520 525  
 Leu His Leu Ser Phe Leu His Val Gln Ile Ile Leu Tyr Arg Pro Phe  
 530 535 540  
 Ile His Tyr Leu Ser Arg Asn Met Asn Ala Glu Asn Val Asp Pro Leu  
 545 550 555 560  
 Cys Tyr Arg Arg Ala Arg Asn Ser Ile Ala Val Ala Arg Thr Val Ile  
 565 570 575  
 Lys Leu Ala Lys Glu Met Val Ser Asn Asn Leu Leu Thr Gly Ser Tyr  
 580 585 590  
 Trp Tyr Ala Cys Tyr Thr Ile Phe Tyr Ser Val Ala Gly Leu Leu Phe  
 595 600 605

Tyr	Ile	His	Glu	Ala	Gln	Leu	Pro	Asp	Lys	Asp	Ser	Ala	Arg	Glu	Tyr
610						615					620				
Tyr	Asp	Ile	Leu	Lys	Asp	Ala	Glu	Thr	Gly	Arg	Ser	Val	Leu	Ile	Gln
625					630					635					640
Leu	Lys	Asp	Ser	Ser	Met	Ala	Ala	Ser	Arg	Thr	Tyr	Asn	Leu	Leu	Asn
				645					650					655	
Gln	Ile	Phe	Glu	Lys	Leu	Asn	Ser	Lys	Thr	Ile	Gln	Leu	Thr	Ala	Leu
			660					665					670		
His	Ser	Ser	Pro	Ser	Asn	Glu	Ser	Ala	Phe	Leu	Val	Thr	Asn	Asn	Ser
		675					680					685			
Ser	Ala	Leu	Lys	Pro	His	Leu	Gly	Asp	Ser	Leu	Gln	Pro	Pro	Val	Phe
	690					695					700				
Phe	Ser	Ser	Gln	Asp	Thr	Lys	Asn	Ser	Phe	Ser	Leu	Ala	Lys	Ser	Glu
705					710					715					720
Glu	Ser	Thr	Asn	Asp	Tyr	Ala	Met	Ala	Asn	Tyr	Leu	Asn	Asn	Thr	Pro
				725					730					735	
Ile	Ser	Glu	Asn	Pro	Leu	Asn	Glu	Ala	Gln	Gln	Gln	Asp	Gln	Val	Ser
			740					745					750		
Gln	Gly	Thr	Thr	Asn	Met	Ser	Asn	Glu	Arg	Asp	Pro	Asn	Asn	Phe	Leu
		755					760					765			
Ser	Ile	Asp	Ile	Arg	Leu	Asp	Asn	Asn	Gly	Gln	Ser	Asn	Ile	Leu	Asp
	770					775					780				
Ala	Thr	Asp	Asp	Val	Phe	Ile	Arg	Asn	Asp	Gly	Asp	Ile	Pro	Thr	Asn
785					790					795					800
Ser	Ala	Phe	Asp	Phe	Ser	Ser	Ser	Lys	Ser	Asn	Ala	Ser	Asn	Asn	Ser
				805					810					815	
Asn	Pro	Asp	Thr	Ile	Asn	Asn	Asn	Tyr	Asn	Asn	Val	Ser	Gly	Lys	Asn
			820					825					830		
Asn	Asn	Asn	Asn	Asn	Ile	Thr	Asn	Asn	Ser	Asn	Asn	Asn	His	Asn	Asn
		835					840					845			
Asn	Asn	Asn	Asp	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn
	850					855					860				
Asn	Asn	Asn	Asn	Asn	Ser	Gly	Asn	Ser	Ser	Asn	Asn	Asn	Asn	Asn	Asn
865					870					875					880
Asn	Asn	Asn	Lys	Asn	Asn	Asn	Asp	Phe	Gly	Ile	Lys	Ile	Asp	Asn	Asn
				885					890					895	
Ser	Pro	Ser	Tyr	Glu	Gly	Phe	Pro	Gln	Leu	Gln	Ile	Pro	Leu	Ser	Gln
			900					905					910		
Asp	Asn	Leu	Asn	Ile	Glu	Asp	Lys	Glu	Glu	Met	Ser	Pro	Asn	Ile	Glu
		915					920					925			
Ile	Lys	Asn	Glu	Gln	Asn	Met	Thr	Asp	Ser	Asn	Asp	Ile	Leu	Gly	Val
	930					935					940				

Phe Asp Gln Leu Asp Ala Gln Leu Phe Gly Lys Tyr Leu Pro Leu Asn  
945 950 955 960

Tyr Pro Ser Glu

<210> 31

<211> 758

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 31

Met Asp Asn Thr Thr Asn Ile Asn Thr Asn Glu Arg Ser Ser Asn Thr  
1 5 10 15

Asp Phe Ser Ser Ala Pro Asn Ile Lys Gly Leu Asn Ser His Thr Gln  
20 25 30

Leu Gln Phe Asp Ala Asp Ser Arg Val Phe Val Ser Asp Val Met Ala  
35 40 45

Lys Asn Ser Lys Gln Leu Leu Tyr Ala His Ile Tyr Asn Tyr Leu Ile  
50 55 60

Lys Asn Asn Tyr Trp Asn Ser Ala Ala Lys Phe Leu Ser Glu Ala Asp  
65 70 75 80

Leu Pro Leu Ser Arg Ile Asn Gly Ser Ala Ser Gly Gly Lys Thr Ser  
85 90 95

Leu Asn Ala Ser Leu Lys Gln Gly Leu Met Asp Ile Ala Ser Lys Gly  
100 105 110

Asp Ile Val Ser Glu Asp Gly Leu Leu Pro Ser Lys Met Leu Met Asp  
115 120 125

Ala Asn Asp Thr Phe Leu Leu Glu Trp Trp Glu Ile Phe Gln Ser Leu  
130 135 140

Phe Asn Gly Asp Leu Glu Ser Gly Tyr Gln Gln Asp His Asn Pro Leu  
145 150 155 160

Arg Glu Arg Ile Ile Pro Ile Leu Pro Ala Asn Ser Lys Ser Asn Met  
165 170 175

Pro Ser His Phe Ser Asn Leu Pro Pro Asn Val Ile Pro Pro Thr Gln  
180 185 190

Asn Ser Phe Pro Val Ser Glu Glu Ser Phe Arg Pro Asn Gly Asp Gly  
195 200 205

Ser Asn Phe Asn Leu Asn Asp Pro Thr Asn Arg Asn Val Ser Glu Arg  
210 215 220

Phe Leu Ser Arg Thr Ser Gly Val Tyr Asp Lys Gln Asn Ser Ala Asn  
225 230 235 240

Phe Ala Pro Asp Thr Ala Ile Asn Ser Asp Ile Ala Gly Gln Gln Tyr  
245 250 255

Ala Thr Ile Asn Leu His Lys His Phe Asn Asp Leu Gln Ser Pro Ala  
260 265 270

000050 223150

Gln	Pro	Gln	Gln	Ser	Ser	Gln	Gln	Ile	Gln	Gln	Pro	Gln	His	Gln	
		275				280					285				
Pro	Gln	His	Gln	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
	290					295					300				
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln
305					310					315					320
Gln	Gln	Gln	His	Gln	Gln	Gln	Gln	Gln	Thr	Pro	Tyr	Pro	Ile	Val	Asn
				325					330					335	
Pro	Gln	Met	Val	Pro	His	Ile	Pro	Ser	Glu	Asn	Ser	His	Ser	Thr	Gly
			340					345					350		
Leu	Met	Pro	Ser	Val	Pro	Pro	Thr	Asn	Gln	Gln	Phe	Asn	Ala	Gln	Thr
	355						360					365			
Gln	Ser	Ser	Met	Phe	Ser	Asp	Gln	Gln	Arg	Phe	Phe	Gln	Tyr	Gln	Leu
	370					375					380				
His	His	Gln	Asn	Gln	Gly	Gln	Ala	Pro	Ser	Phe	Gln	Gln	Ser	Gln	Ser
385					390					395					400
Gly	Arg	Phe	Asp	Asp	Met	Asn	Ala	Met	Lys	Met	Phe	Phe	Gln	Gln	Gln
				405					410					415	
Ala	Leu	Gln	Gln	Asn	Ser	Leu	Gln	Gln	Asn	Leu	Gly	Asn	Gln	Asn	Tyr
			420					425				430			
Gln	Ser	Asn	Thr	Arg	Asn	Asn	Thr	Ala	Glu	Glu	Thr	Thr	Pro	Thr	Asn
		435					440					445			
Asp	Asn	Asn	Ala	Asn	Gly	Asn	Ser	Leu	Leu	Gln	Glu	His	Ile	Arg	Ala
	450					455					460				
Arg	Phe	Asn	Lys	Met	Lys	Thr	Ile	Pro	Gln	Gln	Met	Lys	Asn	Gln	Ser
465					470					475					480
Thr	Val	Ala	Asn	Pro	Val	Val	Ser	Asp	Ile	Thr	Ser	Gln	Gln	Gln	Tyr
				485					490					495	
Met	His	Met	Met	Met	Gln	Arg	Met	Ala	Ala	Asn	Gln	Gln	Leu	Gln	Asn
			500					505					510		
Ser	Ala	Phe	Pro	Pro	Asp	Thr	Asn	Arg	Ile	Ala	Pro	Ala	Asn	Asn	Thr
		515					520					525			
Met	Pro	Leu	Gln	Pro	Gly	Asn	Met	Gly	Ser	Pro	Val	Ile	Glu	Asn	Pro
	530					535					540				
Gly	Met	Arg	Gln	Thr	Asn	Pro	Ser	Gly	Gln	Asn	Pro	Met	Ile	Asn	Met
545					550					555					560
Gln	Pro	Leu	Tyr	Gln	Asn	Val	Ser	Ser	Ala	Met	His	Ala	Phe	Ala	Pro
				565					570					575	
Gln	Gln	Gln	Phe	His	Leu	Pro	Gln	His	Tyr	Lys	Thr	Asn	Thr	Ser	Val
			580					585					590		
Pro	Gln	Asn	Asp	Ser	Thr	Ser	Val	Phe	Pro	Leu	Pro	Asn	Asn	Asn	Asn
		595					600					605			

Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn  
610 615 620

Ser Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Ser Asn Asn  
625 630 635 640

Thr Pro Thr Val Ser Gln Pro Ser Ser Lys Cys Thr Ser Ser Ser Ser  
645 650 655

Thr Thr Pro Asn Ile Thr Thr Thr Ile Gln Pro Lys Arg Lys Gln Arg  
660 665 670

Val Gly Lys Thr Lys Thr Lys Glu Ser Arg Lys Val Ala Ala Ala Gln  
675 680 685

Lys Val Met Lys Ser Lys Lys Leu Glu Gln Asn Gly Asp Ser Ala Ala  
690 695 700

Thr Asn Phe Ile Asn Val Thr Pro Lys Asp Ser Gly Gly Lys Gly Thr  
705 710 715 720

Val Lys Val Gln Asn Ser Asn Ser Gln Gln Gln Leu Asn Gly Ser Phe  
725 730 735

Ser Met Asp Thr Glu Thr Phe Asp Ile Phe Asn Ile Gly Asp Phe Ser  
740 745 750

Pro Asp Leu Met Asp Ser  
755

<210> 32  
<211> 750  
<212> PRT  
<213> Saccharomyces cerevisiae

<400> 32  
Met Thr Ser Val Asn Arg Ser Asn Asn Thr Arg Ser Met Ser Ala Ser  
1 5 10 15

Arg Ser Ala Thr Ser Arg Val Arg Asn Thr Thr Ala Asn Ser Ser Asp  
20 25 30

Val Asn Ser Ser Lys Arg Asn Ser Asn Ser Val Tyr Asp Asp Asn Ser  
35 40 45

Ser Lys Arg Arg Ser Arg Arg Ser Asp Gly Lys Asn Asn Asp His Thr  
50 55 60

Tyr Arg Thr Thr Val Lys Ser Lys Asn Ser Arg Tyr Val Ser Ser Ser  
65 70 75 80

Lys Arg Ala Lys Arg Asn Ser Val Gly Thr Ser Ser Ala Ser Lys Ser  
85 90 95

Ser Asn Gly Gly Ser Ala His Lys Trp Ser Asn Met Lys Asn Val Ser  
100 105 110

Asn Ser Ala Val Asp Ala Gly Ser Asp Ser Lys Ser Val Gly Gly Arg  
115 120 125

Lys Ser Asn Asn Ser Asn Asp Lys Asp Asn Ser Ala Arg Asp Asp Asn  
130 135 140

Asn 145	Ser	Gly	Asn	Asn	Asn 150	Asn	Asn	Asn	Asn	His 155	Ser	Ser	Asn	Asn	Asn 160
Asp	Asn	Asn	Asn	Asn 165	Asn	Asn	Asp	Asp	Asn 170	Asn	Asn	Asn	Asn	Asn	Ser 175
Asn	Ser	Arg	Asp 180	Asn	Asn	Asn	Asn	Ser 185	Asp	Asp	Ser	Asn	Arg 190	Asn	Asp
Ser	Cys	Lys 195	Ala	Ser	Asn	Lys	Arg 200	Ser	Gly	Ala	Lys	Tyr 205	Lys	Val	Val
Lys	Arg 210	Cys	Ser	Thr	Asn	Ser 215	Thr	Thr	Lys	Ser	Trp 220	Thr	Tyr	Lys	Asn
Thr 225	Asp	Val	Asn	Asn	Tyr 230	Val	Thr	Thr	Thr	Ala 235	Ser	His	Asp	Val	Gly 240
Val	Tyr	Arg	Arg	Arg 245	Trp	Val	Tyr	Gly	Thr 250	Thr	Asp	Val	Lys	Asn 255	Ser
Asn	Met	Asp	Val 260	Cys	Cys	Thr	His	Val 265	Val	Ser	Ser	Thr	Met 270	Ser	Asp
Ser	Lys	Tyr 275	Ser	Thr	Trp	Arg	Gly 280	Asp	Ser	Arg	Met	Ala 285	Ala	Tyr	Ser
Ser	Asp 290	Trp	Lys	Ser	Ala	His 295	Trp	Tyr	Thr	Ala	Met 300	Lys	Tyr	Tyr	Asn
His 305	Gly	Lys	Tyr	Tyr	His 310	Met	Ser	Thr	Val	Asn 315	Thr	Ala	Val	Asn	Gly 320
Lys	Ser	Val	Cys	Thr 325	Thr	Ser	Tyr	Met	Val 330	Asp	Asn	Tyr	Arg	Ala 335	Val
Arg	Asn	Asn	Gly 340	Asn	Arg	Asn	Ser	Tyr 345	Lys	His	Ser	Ala	Met 350	Ser	Ser
Asp	Asn	Val 355	Val	Ser	Tyr	Lys	Gly 360	Asp	Ala	Asn	Gly	Cys 365	Asn	Asn	Ala
Asp	Met 370	Val	Asn	Asp	Lys	Tyr 375	Arg	His	Gly	Ser	Ala 380	Ser	His	Val	Gly
Gly 385	Lys	Asn	Ala	Lys	Tyr 390	Lys	Arg	Lys	Asp	Lys	Lys	Arg	Lys	Lys	Ser 400
Ser	Asn	Asn	Asp	Ser 405	Ser	Val	Thr	Ser	Ser 410	Thr	Gly	Asn	Ser	Arg 415	Asn
Asp	Asn	Asp	Asp 420	Asp	Met	Ser	Ser	Thr 425	Thr	Ser	Ser	Asp	His 430	Asp	Ala
Asn	Asp	Asp 435	Thr	Arg	Arg	Ser	Met 440	Thr	Asn	Ala	Trp	Thr 445	Lys	Asn	Met
Thr	Ser 450	Lys	Cys	Gly	Val	Arg 455	Lys	His	Gly	Gly	Ala 460	His	Trp	Tyr	Ser
Cys 465	Lys	Ser	Ser	Ser	Asp 470	Val	Ser	Lys	Trp	Met	Val	Lys	Arg	Ala	Trp 480

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<210> 33
<211> 710
<212> PRT
<213> Saccharomyces cerevisiae
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Asp Arg Asn Asp Thr Arg Met Asn Thr Asn Ala Arg Ser Val Arg Val  
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		35					40					45			
Thr	Arg	Ala	Gly	Arg	Ser	Asp	Thr	Thr	Asn	Ser	Ser	Ala	Lys	His	His
	50					55					60				
Ser	Lys	Lys	Ser	Thr	Val	Val	Val	Val	Thr	Ser	Ser	Thr	Asp	Ser	Asn
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Ser	Thr	Thr	Tyr	Ala	Arg	Val	Ser	Ser	Asp	Ser	Thr	Val	Ala	Thr	Ser
				85					90					95	
Ser	Thr	Thr	Thr	Arg	Thr	Arg	Thr	Arg	Asn	Asn	Thr	Val	Ser	Ser	Thr
			100					105					110		
Ala	Ser	Ser	Ser	Thr	Thr	Asp	Val	Gly	Asn	Ala	Thr	Ser	Ala	Asn	Trp
		115					120					125			
Ser	Ala	Asn	Ala	Ser	Asn	Thr	Ser	Ser	Ser	Asp	Tyr	Ala	Thr	Ser	Tyr
	130					135					140				
Thr	Arg	Lys	Ser	Thr	Asp	Asn	Tyr	Thr	Thr	Ala	Asn	Ser	Lys	Asn	Gly
145					150					155					160
Asn	Asn	Trp	Ser	Ser	Ala	Gly	Asn	Ser	Asn	Thr	Asp	His	Asn	Thr	Val
			165						170					175	
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			180					185					190		
Tyr	Ala	Asn	Tyr	Val	Val	Arg	Val	Lys	Ser	Thr	Ser	Ser	Val	Asp	Asp
	195						200					205			
Val	Asp	Ala	Ser	Asn	Trp	Thr	Ala	Asn	Lys	Val	Val	Asn	Ser	Ala	Thr
	210					215					220				
Asn	Thr	Ser	Ser	Asn	Val	Thr	His	Asn	Ala	Val	Asn	Thr	Ser	Thr	Ser
225					230				235						240
Ala	Thr	Cys	Ser	Tyr	Gly	Lys	Val	Ser	Ala	Arg	Thr	Arg	Gly	Asn	Met
			245						250					255	
Ala	Val	Ser	Thr	Val	Ser	Ala	Cys	Ala	Ala	Gly	Lys	Ser	Lys	Val	Gly
			260					265					270		
Ala	Ser	Thr	Val	Ser	Ala	Arg	Val	Met	Tyr	Asn	Val	Asn	Gly	Asn	Asn
		275					280					285			
Thr	Lys	Asn	His	Gly	Val	Asn	Tyr	Ser	Thr	Ser	Asn	Asn	Thr	Tyr	Cys
	290					295					300				
Asn	Thr	Asn	Ser	His	Ser	Ser	Asn	Asn	Tyr	Ser	Ser	Asp	Ser	Lys	Lys
305					310					315					320
Asp	His	Thr	Ser	Ser	Lys	Tyr	Asp	His	Asn	His	Asn	Ala	Lys	Asn	Lys
				325					330					335	
Gly	Val	Ser	Asp	Thr	Asn	Tyr	Gly	His	Asn	Ser	Lys	Val	Lys	Arg	Lys
			340					345					350		
Asp	Thr	Asp	Ala	Lys	Arg	Arg	Lys	Asp	Ser	Asn	Ser	Ser	Thr	Met	Ala
		355					360					365			



Val 370	Met	Asp	Ser	Ser	Asp	Tyr 375	Gly	Asn	Thr	Val	Lys 380	Asn	Ser	Ser	Asn
Arg 385	Asp	Met	Arg	Lys	Cys 390	Asn	Lys	Tyr	Thr	Ser 395	Met	Gly	Val	His	Lys 400
Asn	Gly	Thr	Trp	Val 405	Cys	Lys	Lys	Met	Ala 410	Asn	Thr	Arg	Asn	Val 415	Thr
Ser	Gly	Val	Ser 420	Asp	Tyr	Cys	Thr	Asn 425	Asp	Gly	Asn	Tyr	Val 430	Gly	Lys
Gly	Trp	Asn 435	Ser	Ser	Val	Ser	His 440	Trp	Thr	Val	Asn	Arg 445	Tyr	Gly	Ser
Arg	Ala 450	Val	Arg	Ala	Cys	Ala 455	Asp	Ser	Thr	Cys	Thr 460	Thr	Ser	Val	Ser
Tyr 465	Ala	Thr	Asp	Thr	Asn 470	Gly	Thr	Thr	Trp	Asp 475	Thr	Cys	Thr	Asn	Lys 480
Asn	Cys	Asp	Lys	Val 485	Asn	Lys	Asn	Val	Lys 490	Cys	Cys	His	Lys	Gly 495	Ser
Thr	Val	Lys	Asn 500	Arg	Gly	Gly	Ala	Ser 505	Lys	Asn	Lys	His	Ala 510	Asp	Gly
Ser	Ser	Asp 515	Ser	Asp	Gly	Asn	Tyr 520	Gly	Thr	Tyr	Lys	Val 525	Thr	Ser	Arg
Asp	Asn 530	Ser	Val	Arg	Asp	Ala 535	Thr	Lys	Arg	Asn	Ser 540	Asn	Asn	Ser	Arg
Val 545	Gly	Ser	Ser	Ala	Gly 550	Ser	Lys	Ser	Ser	Lys 555	Asn	His	Arg	Lys	His 560
Gly	His	Ser	Gly	Arg 565	Ala	Arg	Gly	Val	Ser 570	Val	Ser	Ser	Val	Arg 575	Ser
Ser	Asn	Ser	Arg 580	His	Asn	Ser	Val	Met 585	Asn	Asn	Ala	Gly	Thr 590	Ala	Asn
Asn	Ala 595	Met	Ser	Asn	Ser	Tyr	Asn 600	Asn	Val	Val	Tyr	Ser 605	Gly	Asn	Asn
Asn	Asn 610	Gly	Asn	Ser	Asn	Gly 615	Asp	Asn	Ser	Asp	Ser 620	Arg	Ala	Asn	Gly
Thr 625	Asn	Ser	Val	Asn 630	Asn	Val	Ser	Asn	Asn	Asn 635	Asn	Asn	Tyr	Asn	Asn 640
Ser	Gly	Tyr	Ser	Ser 645	Met	Asn	Ser	Arg	Ser 650	Val	Ser	His	Asn	Asn 655	Asn
Asn	Asn	Thr	Asn 660	Asn	Tyr	Asn	Asn	Asn 665	Asp	Asn	Asp	Asn	Asn 670	Asn	Asn
Asn	Asn	Asn 675	Asn	Asn	Asn	Asn	Asn 680	Asn	Asn	Asn	Asn	Asn 685	Asn	Asn	Asn
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<210> 34
<211> 477
<212> PRT
<213> Saccharomyces cerevisiae
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Arg	Arg	Tyr	Arg	Tyr	Val	Ser	Gly	Ser	Val	Ser	Gly	Lys	Arg	Trp	Thr
			20					25					30		
Asp	Gly	Val	Ser	Trp	Ser	Ser	Arg	Ser	Gly	Lys	Tyr	Lys	Asp	Lys	Asn
		35					40					45			
Ala	Gly	Ser	Asn	Ala	Asn	Ala	Thr	Ser	Ser	Gly	Ser	Thr	Asp	Ser	Ala
	50					55					60				
Val	Thr	Asp	Gly	Thr	Ser	Gly	Ala	Arg	Asn	Asn	Ser	Ser	Ser	Lys	Lys
65					70					75					80
Lys	Asn	His	Asp	Thr	Met	Gly	His	Ser	Ser	Ser	Asp	Thr	Ser	Ser	Ser
				85					90					95	
Asn	Arg	Ser	Asn	Lys	Tyr	Thr	Gly	Val	Lys	Lys	Thr	Ser	Val	Lys	Lys
			100					105					110		
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		115					120					125			
Val	Thr	Lys	Ala	Ser	Lys	Asp	Val	Arg	Ser	Val	Ala	Met	Gly	Asn	Thr
	130					135					140				
Thr	Gly	Asn	Val	Lys	Asn	Asn	Ser	Thr	Thr	Thr	Gly	Asn	Gly	Asn	Asn
145					150					155					160
Asn	Asn	Lys	Ser	Asn	Ser	Ser	Thr	Asn	Thr	Val	Ser	Thr	Asn	Asn	Asn
				165					170					175	
Ser	Ala	Asn	Asn	Ala	Ala	Gly	Ser	Asn	Thr	Ser	Ala	Asn	Lys	Asn	Tyr
		180					185						190		
Tyr	Tyr	Lys	Asn	Asp	Ser	Ser	Gly	Tyr	Thr	Ala	Ala	Ser	Thr	Thr	Met
		195					200				205				
Tyr	Thr	Ala	Asn	Tyr	Thr	Ser	Asp	Asn	Thr	Asn	Ala	Thr	Gly	Met	Asn
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Thr	His	Val	Asn	Asn	Asn	Asn	Asn	Asn	Ser	Asn	Asn	Ser	Ser	Asn	Ser
225					230					235					240
Asn	Asn	Ser	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn
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Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Val	Asn	Thr	Asn	Ala	Gly	Asn	Gly
			260					265					270		
Asn	Asn	Asn	Arg	His	Asn	Ala	Ser	Ala	Tyr	Asn	Thr	Thr	Gly	Asp	Asn
		275					280						285		

Tyr Asp Ser Lys Ser Lys Val Thr Asn Cys Asp His Lys Ala Ser Ser  
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His	Ser	Met	Lys	Tyr	Lys	Lys	Arg	Ser	Val	Asp	Lys	Asp	His	Val	Met
		115					120					125			
Lys	Asp	Asp	Ser	Ser	Val	Lys	Ala	Ser	Lys	Met	Asn	Ser	His	Asn	Tyr
	130					135					140				
Ser	Thr	Asn	Thr	Met	Asn	Lys	Met	Asp	Val	Tyr	Thr	Lys	Ala	Asn	Met
145					150					155					160
Ala	Asn	Lys	Lys	Lys	Ser	Asp	Thr	Ser	Thr	Trp	Lys	Asn	Lys	Asn	Lys
				165					170					175	
Ser	His	Val	Ser	Tyr	Asn	Asn	Asp	Lys	Ser	Lys	Thr	Lys	Trp	Tyr	Asn
			180					185					190		
Asp	Ser	Asp	Asp	Asp	Asp	Asp	Asn	Asn	Val	Asn	Asn	Asn	Asp	Asn	Asn
		195					200					205			
Asn	Asn	Asn	Lys	Asn	Asp	Asn	Asn	Asn	Asp	Asn	Asn	Asn	Asp	Thr	Ser
		210				215						220			
Asn	Asn	Asn	Asn	Asn	Asn	Asn	Asn	Arg	Thr	Lys	Asn	Asn	Arg	Asn	Asn
225					230					235					240
Arg	Asp	Trp	Lys	Thr	Lys	Lys	Cys	Thr	Asp	Met	Asn	Asp	Lys	Arg	Asp
				245					250					255	
Asn	Asn	Asn	Lys	Asn	Asp	Met	Ala	Arg	Asn	Asp	Asn	Lys	Asn	Tyr	Asn
			260					265					270		
Asn	Val	Asn	Lys	Arg	Asn	His	Lys	Ser	Ser	Cys	Arg	Arg	Asp	Gly	Tyr
		275					280					285			
Ser	Ala	Asn	Asn	Ala	Val	Asn	Ser	Thr	His	Ala	Ser	Asn	Lys	Asn	Val
	290					295					300				
Asn	Asp	Met	Asn	Asn	Asp	Thr	Tyr	Lys	Asn	Lys	Thr	Asp	Thr	Asn	Lys
305					310					315					320
Lys	Asn	Asp	Ser	Asn	Ser	Asn	Asp	Val	Thr	Arg	Lys	Lys	Arg	Lys	Thr
				325					330					335	
Ser	Asp	Gly	Asn	Tyr	Ser	Arg	Asn	Asn	Val	Ser	Val	Ser	Arg	Ser	Lys
			340					345					350		
Ala	Thr	Thr	Lys	Lys	Thr	Lys	Lys	Lys	Lys	Arg	Arg	Asp	Gly	Lys	Asp
			355					360							
Lys	Lys	Asn	Lys	Lys	Asn	Ala	Asp	Asn	Lys	Lys	Asn	Asn	Ala	Val	Thr
	370					375					380				
Val	Ser	Val	Tyr	Asp	Ser	Asn	Lys	Val	Lys	Ser	Asn	Lys	Arg	Ser	Arg
385					390					395					400
Lys	Val	Asn	Asn	Lys	Ser	Asp	Val	Val	Asn	Ser	Gly	Lys	Asp	Ser	Arg
				405					410					415	
Val	Lys	Ser	Cys	Lys	Lys	Tyr	Ala	Asp	Asn	Asn	Thr	Lys	Ser	Asn	Asp
			420					425					430		
Ala	Asp	Gly	Trp	Asp	Asp	Met	Asn	Trp	Val	Asp	Arg	Gly	Cys	Ala	Thr
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Asn	Thr	Asn	Lys	Arg	His	Lys	Asn	Ala	Ser	Asn	Asp	Arg	Asp	Ser	Val
			20					25					30		
Ser	Ser	Asn	Thr	Thr	Ser	Met	Thr	Asp	Asp	Ala	Asp	Tyr	Asn	Gly	Ala
		35					40					45			
Ser	Arg	Thr	Lys	Asn	Asn	Ser	Asp	Ser	Asp	Arg	Ser	Asn	Asp	Thr	Lys
	50					55					60				
Asn	Asn	Tyr	Asn	Lys	Arg	Thr	Gly	Tyr	Asn	Tyr	Asn	Gly	Ser	Gly	Asn
65					70					75					80
Arg	Tyr	Thr	Arg	Lys	Arg	Thr	Ala	Asn	Lys	Ala	Tyr	Ser	Asp	Asp	Asn
				85					90					95	
Val	Lys	Asp	Asp	Asn	Asn	Thr	Lys	Lys	Ala	Ser	Arg	Ser	Ser	Gly	Arg
			100					105					110		
Asn	Val	Asn	Thr	Arg	Asn	Lys	Ser	Lys	Ser	His	Lys	Val	Lys	Asn	Asn
		115					120					125			
Lys	Ser	Ser	Ser	Arg	Lys	Ser	Ser	Ala	Ala	Arg	Lys	Gly	Lys	Tyr	Asn
	130					135					140				
Ser	Asn	Ser	Asp	Ser	Thr	Thr	Arg	Lys	Val	Thr	Asp	Val	Lys	Lys	Arg
145					150					155					160
Ser	Lys	Trp	His	Arg	His	Asp	Lys	Lys	Met	Val	Lys	Lys	Ser	Arg	Tyr
			165						170					175	
Arg	Lys	Arg	Met	Arg	Gly	Thr	Asp	Val	Ser	Ser	Ser	Asp	Asn	Ser	Lys
			180					185					190		
Ser	Thr	Thr	Lys	Ser	Tyr	Val	Ser	Lys	Asn	Ser	Ala	Met	Asn	Asn	Asn
		195					200					205			
Asp	Val	Thr	Asp	Asn	Lys	Lys	Thr	Asn	Asn	Asn	Lys	Ala	Arg	Asp	Ser
	210					215					220				
Met	His	Thr	Lys	Lys	Asp	Thr	Lys	Asp	Asp	Thr	Asp	Ser	Lys	Lys	Arg
225					230					235					240
Lys	Val	Val	Thr	Asn	Asp	Asn	Ala	Ala	Met	Val	Asn	Lys	Gly	Trp	Arg
				245					250					255	
Lys	Asn	Val	Met	Met	Tyr	Lys	Lys	Ser	Gly	Asn	Met	Lys	Lys	Tyr	Arg
			260					265					270		
Tyr	Trp	Thr	Cys	Tyr	Cys	Asn	Tyr	Val	Tyr	Tyr	Arg				
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<210> 37  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 37  
gggaattccc attaccgaca tttgggcgc 29

<210> 38  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 38  
ggggattctg attgattgat tgattgtac 29

<210> 39  
<211> 720  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: superbright  
GFP encoding sequence

<220>  
<221> CDS  
<222> (1)..(720)

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Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
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ggt gaa tta gat ggt gat gtt aat ggg cac aaa ttt tct gtc agt gga 96  
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30  
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att 144  
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45  
tgc act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act 192  
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60  
ttc act tat ggt gtt cag tgc ttt tca aga tac ccg gat cat atg aaa 240  
Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80  
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288  
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

006050:223656

aga act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa 336  
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384  
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly  
115 120 125

att gat ttt aaa gaa gat gga aac att ctt ggg cac aaa ttg gaa tac 432  
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr  
130 135 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480  
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn  
145 150 155 160

gga atc aaa gct aac ttc aaa att aga cac aac att gaa gat gga agc 528  
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser  
165 170 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576  
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly  
180 185 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624  
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu  
195 200 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672  
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe  
210 215 220

gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa tga 720  
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys  
225 230 235 240

<210> 40

<211> 239

<212> PRT

<213> Artificial Sequence

<400> 40

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu  
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Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly  
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile  
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr  
50 55 60

Phe Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys  
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu  
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu  
100 105 110

005050:225550

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<210> 44
<211> 36
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34



<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

ggaccgcggg tagcggttct gttgagaaaa gttgcc

36

<210> 45

<211> 7239

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: vector  
containing chimeric gene

<400> 45

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cttaggacgg atcgcttgcc tgtaacttac acgcgcctcg tatcttttaa tgatggaata 120  
at ttggaat ttactctgtg tttatttatt tttatgtttt gtatttggat tttagaaagt 180  
aaataaagaa ggtagaagag ttacggaatg aagaaaaaaa aataaacaaa ggtttaaaaa 240  
at ttcaacaa aaagcgtact ttacatatat at ttattaga caagaaaagc agattaaata 300  
gatatacatt cgattaacga taagtaaaat gtaaaatcac aggattttcg tgtgtggtct 360  
tctacacaga caagatgaaa caattcggca ttaataacctg agagcaggaa gagcaagata 420  
aaaggtagta tttgttgggc atccccctag agtcttttac atcttcggaa aacaaaaact 480  
at ttttttctt taatttcttt ttttactttc tatttttaat ttatatattt atattaaaaa 540  
at tttaaatta taattatttt tatagcacgt gatgaaaagg acccaggtgg cacttttcgg 600  
ggaaatgtgc gcggaacccc tatttgttta tttttctaaa tacattcaaa tatgtatccg 660  
ctcatgagac aataaccctg ataaatgctt caataatatt gaaaaaggaa gagtatgagt 720  
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<212> PRT
<213> Pichia pinus
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<212> PRT
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Ala Gln Ser Phe Val Pro Gln Gly Gly Tyr Gln Gln Phe Gln Gln Phe
 35           40           45
Gln Pro Gln Gln Gln Gln Gln Gln Tyr Gly Gly Tyr Asn Gln Tyr Asn
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Gln Gln Tyr Asn Ser Gln Pro Gln Gln Gln Gln Gln Gln Ser Gln
115          120          125
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Ser Leu Asn Lys Pro Ala Val Lys Lys Thr Leu Lys Leu Ala Gly Ser
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Val Lys Lys Gly Thr Asn Leu Ile Met Met Pro Asn Lys Thr Pro Ile  
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<211> 7988

<212> DNA

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<220>

<223> Description of Artificial Sequence: Ure2N-Sup35C  
integration plasmid

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gatgatgccg agggaagcag cgaaggacca aaggacaaaa aaacaactgg ttctttgagt 2520  
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gttggtagcc ttttctaatt tgtgcaataa cttaacaata tgtacctt caattgctgt 3060

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atgaacatgc ataacacatg aaaaaccggc tgctatgata gattttaatt ctacaatagc 3120  
aatttgagct acaaacttgg taacactctt gatagggttc tttggcgatg ttagtacaaa 3180  
acctggtgaa atgtcttctt cttcaacacc tttgattctt agtttaactt gctcaccaca 3240





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<210> 50
<211> 405
<212> PRT
<213> Saccharomyces cerevisiae

<400> 50
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Gly Asn His Ala Glu Ala Val Ala Lys Leu Thr Ser Ala Ala Gln Ser
          20          25          30
Asn Pro Asn Asp Glu Gln Met Ser Thr Ile Glu Ser Leu Ile Gln Lys
          35          40          45
Ile Ala Gly Tyr Val Met Asp Asn Arg Ser Gly Gly Ser Asp Ala Ser
  50          55          60
Gln Asp Arg Ala Ala Gly Gly Gly Ser Ser Phe Met Asn Thr Leu Met
  65          70          75          80
Ala Asp Ser Lys Gly Ser Ser Gln Thr Gln Leu Gly Lys Leu Ala Leu
          85          90          95
-Leu-Ala-Thr-Val-Met-Thr-His-Ser-Ser-Asn-Lys-Gly-Ser-Ser-Asn-Arg-
          100          105          110
Gly Phe Asp Val Gly Thr Val Met Ser Met Leu Ser Gly Ser Gly Gly
          115          120          125

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<210>	51
<211>	128
<212>	PRT

<400> 51

Met Ser Ala Asn Asp Tyr Tyr Gly Gly Thr Ala Gly Glu Lys Ser Gln  
1 5 10 15

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<210> 52
<211> 534
<212> PRT
<213> Saccharomyces cerevisiae
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Thr	Lys	Glu	Glu	Arg	Ser	Lys	Ala	Asp	Leu	Ser	Lys	Glu	Ser	Cys	Lys
145					150					155					160
Met	Phe	Ile	Gly	Gly	Leu	Asn	Trp	Asp	Thr	Thr	Glu	Asp	Asn	Leu	Arg
				165					170					175	



Glu 180	Tyr	Phe	Gly 180	Lys	Tyr	Gly	Thr 185	Val	Thr	Asp	Leu	Lys 190	Ile	Met	Lys
Asp 195	Pro	Ala 195	Thr	Gly	Arg	Ser	Arg 200	Gly	Phe	Gly	Phe	Leu 205	Ser	Phe	Glu
Lys 210	Pro	Ser	Ser	Val	Asp	Glu 215	Val	Val	Lys	Thr	Gln 220	His	Ile	Leu	Asp
Gly 225	Lys	Val	Ile	Asp	Pro 230	Lys	Arg	Ala	Ile	Pro 235	Arg	Asp	Glu	Gln	Asp 240
Lys	Thr	Gly	Lys 245	Ile	Phe	Val	Gly	Gly 250	Ile	Gly	Pro	Asp	Val	Arg 255	Pro
Lys	Glu	Phe	Glu 260	Glu	Phe	Phe	Ser	Gln 265	Trp	Gly	Thr	Ile	Ile 270	Asp	Ala
Gln	Leu	Met 275	Leu	Asp	Lys	Asp	Thr 280	Gly	Gln	Ser	Arg	Gly 285	Phe	Gly	Phe
Val	Thr 290	Tyr	Asp	Ser	Ala	Asp 295	Ala	Val	Asp	Arg	Val 300	Cys	Gln	Asn	Lys
Phe 305	Ile	Asp	Phe	Lys	Asp 310	Arg	Lys	Ile	Glu	Ile 315	Lys	Arg	Ala	Glu	Pro 320
Arg	His	Met	Gln 325	Gln	Lys	Ser	Ser	Asn	Asn 330	Gly	Gly	Asn	Asn	Gly 335	Gly
Asn	Asn	Met 340	Asn	Arg	Arg	Gly	Gly	Asn 345	Phe	Gly	Asn	Gln	Gly 350	Asp	Phe
Asn	Gln	Met 355	Tyr	Gln	Asn	Pro	Met 360	Met	Gly	Gly	Tyr	Asn 365	Pro	Met	Met
Asn	Pro 370	Gln	Ala	Met	Thr	Asp 375	Tyr	Tyr	Gln	Lys	Met 380	Gln	Glu	Tyr	Tyr
Gln 385	Gln	Met	Gln	Lys	Gln 390	Thr	Gly	Met	Asp	Tyr 395	Thr	Gln	Met	Tyr	Gln 400
Gln	Gln	Met	Gln 405	Gln	Met	Ala	Met	Met 410	Met	Pro	Gly	Phe	Ala	Met 415	Pro
Pro	Asn	Ala 420	Met	Thr	Leu	Asn	Gln 425	Pro	Gln	Gln	Asp	Ser	Asn 430	Ala	Thr
Gln	Gly 435	Ser	Pro	Ala	Pro	Ser	Asp 440	Ser	Asp	Asn	Asn	Lys 445	Ser	Asn	Asp
Val 450	Gln	Thr	Ile	Gly	Asn	Thr 455	Ser	Asn	Thr	Asp	Ser 460	Gly	Ser	Pro	Pro
Leu 465	Asn	Leu	Pro	Asn	Gly 470	Pro	Lys	Gly	Pro	Ser 475	Gln	Tyr	Asn	Asp	Asp 480
His	Asn	Ser	Gly 485	Tyr	Gly	Tyr	Asn	Arg	Asp 490	Arg	Gly	Asp	Arg	Asp 495	Arg
Asn	Asp	Arg 500	Asp	Arg	Asp	Tyr	Asn	His 505	Arg	Ser	Gly	Gly	Asn 510	His	Arg



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<210> 58
<211> 22
<212> DNA
<213> Artificial Sequence
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<400> 58  
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<210> 59
<211> 34
<212> DNA
<213> Artificial Sequence
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<400> 59  
ggaggatcca tggatacggg taagttaatc tcag 34

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<210> 60
<211> 36
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: primer

<400> 60  
ggaccgcggg tagcggttct gttgagaaaa gttgcc 36

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<210> 61
<211> 36
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Description of Artificial Sequence: primer

<400> 61  
gaggatccat gcctgatgat gaggaagaag acgagg 36

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<210> 62
<211> 26
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: primer

<400> 62  
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<400> 63  
gggatcctgt tgctagtggg caga

24

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<220>
<223> Description of Artificial Sequence: primer
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```
<400> 64
gtaccgcgga tgtctttgaa cgactttcaa aagc
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34

<220>  
<223> Description of Artificial Sequence: primer

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<400> 65
gtggagctct tactcggcaa ttttaacaat tttac
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35